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No> Frazer, Ian Hector

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
20 25 30

tot gto ago gga gag ggt gaa ggt gat goo aca tao gga aag oto aco 144 Ser Val Ser Glv Glu Glv Glv Asp Ala Thr Tvr Glv Lvs Leu Thr

Ser Val Ser Gly Glu Gly Glu Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288

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	_	_	_	_	aag Lys		_		_		_			_		384
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

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		t tat caa cag aac act s Tyr Gln Gln Asn Thr 190	
		c aac cat tac ctg tcc p Asn His Tyr Leu Ser 205	
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Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
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Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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			ctg Leu							576
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Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
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140

135

130

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					_	ctg Leu	_	_				_				576
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Glu Asp Gly	Ser Val Gln 180	Leu Ala Asp 185	His Tyr Gln Gln	Asn Thr Pro 190
Ile Gly Asp 195		Leu Leu Pro 200	Asp Asn His Tyr 205	Leu Ser Thr
Gln Ser Ala 210	Leu Ser Lys	Asp Pro Asn 215	Glu Lys Arg Asp 220	His Met Val
Leu Leu Glu 225	Phe Val Thr 230	Ala Ala Gly	Ile Thr His Gly 235	Met Asp Glu 240
Leu Tyr Lys				
<210> 13 <211> 732 <212> DNA <213> Artif	icial Sequend	ce		
<220> <223> Descr	iption of Art	cificial Seq	uence: Arg(CGA)50	;FP
<220> <221> CDS <222> (1)	(732)			
	_		gag gaa ctg ttc Glu Glu Leu Phe 10	
gtc cca att Val Pro Ile	ctc gtg gaa Leu Val Glu 20	ctg gat ggc Leu Asp Gly 25	gat gtg aat ggg Asp Val Asn Gly	cac aaa ttt 96 His Lys Phe 30
			gcc aca tac gga Ala Thr Tyr Gly 45	

60

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

55

50

ctg Leu 65																240
gac Asp		_	_	_		-			_	_	-	_				288
tat Tyr		_		_						_	_				_	336
acc Thr	_	_	_	_	_		_		_		_			_		384
gag Glu	_	_			_		_		_							432
aag Lys 145	_	_											_	_	_	480
aag Lys		_				_	_			_		_				528
gag Glu	-				_	_	_	_				_				576
atc (-							_				_			624
cag Gln			-			_			_	_	_	-		_	_	672
ctg Leu 225																720
ctg Leu		_	tga													732
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<220	>															

<223> Description of Artificial Sequence: Arg(CGA)5GFP

<400> 14

Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 15

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGC)5GFP

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cag tot goo otg tot aaa gat ooc aac gaa aag aga gac cac atg gto Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 230 235 ctg tac aag tga 732 Leu Tyr Lys <210> 16 <211> 243 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Arg(CGC)5GFP <400> 16 Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 120 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

185

Ile Gly Asp Gly 195	Pro Val Le	u Leu Pro Asp 200	Asn His Tyr I 205	eu Ser Thr
Gln Ser Ala Leu 210	Ser Lys As 21	_	Lys Arg Asp H 220	is Met Val
Leu Leu Glu Phe 225	Val Thr Al 230	a Ala Gly Ile	Thr His Gly M 235	Iet Asp Glu 240
Leu Tyr Lys				
<210> 17 <211> 732 <212> DNA <213> Artificia	l Sequence			
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<220> <221> CDS <222> (1)(732)			
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gtc cca att ctc Val Pro Ile Leu 20	Val Glu Le			
tct gtc agc gga Ser Val Ser Gly 35				
ctg aaa ttc atc Leu Lys Phe Ile 50		r Gly Lys Leu		
ctg gtc act acc Leu Val Thr Thr 65				
gac cat atg aag Asp His Met Lys			Ser Ala Met P	
tat gtg cag gag Tyr Val Gln Glu 100	Arg Thr Il		Asp Asp Gly A	
acc cgc gct gaa Thr Arg Ala Glu 115				

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly 130 135 140	
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala 145 150 155	-
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn 165 170 175	
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr 180 185 190	
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser 195 200 205	
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met 210 215 220	
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp 230 235	
ctg tac aag tga Leu Tyr Lys	732
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys 20 25 30	Phe
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu 35 40 45	Thr
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro 50 55 60	Thr
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr 65 70 75	Pro 80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu	

				85					90					95		
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
)> 19 L> 73															
	2> Di 3> Ai		icial	l Sec	quenc	ce										
<220> <223> Description of Artificial Sequence: Arg(CGT)5GFP																
	L> CI		(732))												
)> 19 cat		cat	cat	cat	agc	aaq	aac	gag	gaa	cta	ttc	act	ggc	ata	48
														Gly 15		
														aaa Lys		96

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

_				_		act Thr 55		_								192
						tat Tyr										240
						gac Asp			_	_		_				288
						atc Ile										336
				_		ttc Phe	_		_		_			_		384
						ttt Phe 135									cac His	432
						aac Asn							_	-	-	480
						aag Lys	-			_		-				528
					_	ctg Leu	_	_				_				576
Ile	Gly	Asp 195	Gly	Pro	Val	ctc Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	624
						gat Asp 215										672
						gct Ala										720
_	tac Tyr	aag Lys	tga													732
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<211> 243 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Arg(CGT)5GFP

<400> 20

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 21

<211> 732

<212> DNA

<213> Artificial Sequence

<220> <223> Description of Artificial Sequence: Asn(AAC)5GFP												
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30												
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45												
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60												
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80												
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95												
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110												
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125												
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140												
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160												
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175												
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190												
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624												

Ile Gly Asp Gly	/ Pro Val Le	u Leu Pro 200	_	yr Leu Ser 05	Thr								
cag tot goo otg Gln Ser Ala Let 210		p Pro Asn											
ctg ctg gag ttt Leu Leu Glu Pho 225													
ctg tac aag tga Leu Tyr Lys	ı				732								
<210> 22 <211> 243 <212> PRT <213> Artificial Sequence													
<220> <223> Descripti	on of Artif	icial Sequ	Sequence: Asn(AAC)5GFP										
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Val Pro Ile Let		u Asp Gly	Asp Val Asn G	ly His Lys 30	Phe								
Ser Val Ser Gly	Glu Gly Gl	u Gly Asp . 40	Ala Thr Tyr G	ly Lys Leu 45	Thr								
Leu Lys Phe Ile	e Cys Thr Th 5		Leu Pro Val P 60	ro Trp Pro	Thr								
Leu Val Thr Thi	Phe Ser Ty	r Gly Val	Gln Cys Phe S 75	er Arg Tyr	Pro 80								
Asp His Met Lys	Gln His As 85	o Phe Phe	Lys Ser Ala M 90	et Pro Glu 95	Gly								
Tyr Val Gln Glu 100		e Phe Phe 1	Lys Asp Asp G	ly Asn Tyr 110	Lys								
Thr Arg Ala Glu	ı Val Lys Ph	e Glu Gly 2 120	=	al Asn Arg 25	Ile								
Glu Leu Lys Gly	Ile Asp Pho		Asp Gly Asn I 140	le Leu Gly	His								
Lys Leu Glu Tyr 145	Asn Tyr Asi	n Ser His	Asn Val Tyr I 155	le Met Ala	Asp 160								
Lys Gln Lys Asr	Gly Ile Ly		Phe Lys Ile A 170	rg His Asn 175	Ile								

Glu Asp Gly Ser 180	Val Gln Leu Ala	Asp His Tyr Gln 185	Gln Asn Thr Pro 190										
Ile Gly Asp Gly 195	Pro Val Leu Leu 200	Pro Asp Asn His	Tyr Leu Ser Thr 205										
Gln Ser Ala Leu 210	Ser Lys Asp Pro 215	Asn Glu Lys Arg 220	Asp His Met Val										
Leu Leu Glu Phe 225	Val Thr Ala Ala 230	Gly Ile Thr His 235	Gly Met Asp Glu 240										
Leu Tyr Lys													
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<220> <221> CDS <222> (1)(732)													
		ggc gag gaa ctg											
Met Asn Asn Asn 1	Asn Asn Ser Lys 5	Gly Glu Glu Leu 10	Phe Thr Gly Val 15										
gtc cca att ctc Val Pro Ile Leu 20	gtg gaa ctg gat Val Glu Leu Asp	ggc gat gtg aat Gly Asp Val Asn 25	ggg cac aaa ttt 96 Gly His Lys Phe 30										
		gat gcc aca tac Asp Ala Thr Tyr											
		aag ctc cct gtg Lys Leu Pro Val 60											
		gtg cag tgc ttt Val Gln Cys Phe 75											
		ttc aag agc gcc Phe Lys Ser Ala 90											
		ttc aaa gat gac Phe Lys Asp Asp 105											
acc cgc gct gaa	gtc aag ttc gaa	ggt gac acc ctg	gtg aat aga atc 384										

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 4 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	132
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 4 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	180
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 5 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 5 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 6 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	524
cag tot goo otg tot aaa gat ooc aac gaa aag aga gac cac atg gto 6 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	72
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 7 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	20
ctg tac aag tga 7 Leu Tyr Lys	32
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<220> <223> Description of Artificial Sequence: Asn(AAT)5GFP	
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro	

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

105

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 25

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC)5GFP

<220>

<221> CDS

<222> (1)..(732)

<400> 25

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Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144

Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
														cca Pro		192
														tac Tyr		240
				_		_			_	-	-	_		gag Glu 95		288
		_		_						_	_			tac Tyr	_	336
														aga Arg		384
	-	_			-		_		-					ggc Gly		432
													_	gcc Ala	-	480
						_	-			_		_		aac Asn 175		528
					_	_	_	_				_		act Thr		576
														tcc Ser		624
														atg Met		672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_	tac Tyr	aag Lys	tga													732

<210> 26 <211> 243 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC)5GFP

<400> 26

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1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 27 <211> 732

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<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Asp(GAT)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 27
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Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
                              40
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aqa tac cca
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65
                     70
                                          75
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
acc ege get gaa gte aag tte gaa ggt gae acc etg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                    150
                                         155
                                                             160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
                                                                   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165
                                                         175
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca
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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

180	185		190
atc ggc gac ggc cct Ile Gly Asp Gly Pro 195	(E)	-	-
cag tct gcc ctg tct Gln Ser Ala Leu Ser 210	-		
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ctg tac aag tga Leu Tyr Lys			732
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Ser Val Ser Gly Glu 35	Gly Glu Gly Asp 40	Ala Thr Tyr Gly	Lys Leu Thr
Leu Lys Phe Ile Cys 50	Thr Thr Gly Lys 55	Leu Pro Val Pro 60	Trp Pro Thr
Leu Val Thr Thr Phe 65	Ser Tyr Gly Val 70	Gln Cys Phe Ser . 75	Arg Tyr Pro 80
Asp His Met Lys Gln 85	His Asp Phe Phe	Lys Ser Ala Met : 90	Pro Glu Gly 95
Tyr Val Gln Glu Arg 100	Thr Ile Phe Phe 105		Asn Tyr Lys 110
Thr Arg Ala Glu Val 115	Lys Phe Glu Gly	Asp Thr Leu Val 1	Asn Arg Ile
Glu Leu Lys Gly Ile 130	Asp Phe Lys Glu . 135	Asp Gly Asn Ile 1	Leu Gly His
Lys Leu Glu Tyr Asn 145	Tyr Asn Ser His . 150	Asn Val Tyr Ile 1 155	Met Ala Asp 160

Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val.	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Leu Tyr Lys															
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						ctg Leu										96
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ctg Leu				_		act		_								192
	Lys ₋ 50	Pne	iie	Cys	Thr	55	GIŸ	БуБ	Deu	110	60	PIO				
	_50	act	acc	ttc	tct		ggc	gtg	cag	tgc	60 ttt	tcc	aga	tac	cca	240
Leu 65 gac	_50 gtc Val	act Thr	acc Thr	ttc Phe cag	tct Ser 70	55 tat	ggc Gly ttt	gtg Val	cag Gln aag	tgc Cys 75 agc	60 ttt Phe gcc	tcc Ser atg	aga Arg	tac Tyr gag	cca Pro 80 ggc	240

100 105 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc qqc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 175 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro ate gge gae gge cet gtg ete ete eea gae aae eat tae etg tee aee Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 200 cag tot goo otg tot aaa gat ooc aac gaa aag aga gac cac atg gto Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 215 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

ctg tac aag tga 732 Leu Tyr Lys

<210> 30

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cys(TGC)5GFP

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1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys <210> 31 <211> 732 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Cys(TGT)5GFP <220> <221> CDS <222> (1)..(732) <400> 31 atg tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg Met Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 15 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96

55

60

50

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe

tct	atc	agc	gga	gag	aat.	даа	aat	gat	acc	aca	tac	gga	ааσ	ctc	acc	144
														Leu		
														cca Pro		192
									_	_			_	tac Tyr		240
_		_	_	_		_			_	_	-	_		gag Glu 95		288
		_		_						_	_			tac Tyr	-	336
														aga Arg		384
														ggc Gly		432
										-			_	gcc Ala		480
														aac Asn 175		528
	Asp		Ser	Val		Leu		Asp	His	Tyr	Gln	Gln	Asn	act Thr		576
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	tac Tyr	_	tga													732

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Leu Tyr Lys

225

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

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<213> Artificial Sequence
<223> Description of Artificial Sequence: Gln(CAA)5GFP
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
                         55
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65
                     70
                                         75
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                           120
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                       135
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                    150
                                        155
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arq His Asn Ile
                165
                                    170
                                                        175
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Glu Asp Gly			ctg gcc Leu Ala									576
atc ggc gac Ile Gly Asp 195	Gly Pro											624
cag tct gcc Gln Ser Ala 210		Lys A										672
ctg ctg gag Leu Leu Glu 225												720
ctg tac aag Leu Tyr Lys	_											732
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Met Gln Gln	5			_	10					15		
Met Gln Gln 1	Leu Val 20	Glu I	Leu Asp	Gly 25	10 Asp	Val	Asn	Gly	His 30	15 Lys	Phe	
Met Gln Gln 1 Val Pro Ile Ser Val Ser	Leu Val 20 Gly Glu	Glu I Gly C	Leu Asp Glu Gly 40	Gly 25 Asp	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val	Gly Gly 45	His 30 Lys	15 Lys Leu	Phe Thr	
Met Gln Gln 1 Val Pro Ile Ser Val Ser 35 Leu Lys Phe	Leu Val 20 Gly Glu Ile Cys	Glu I	Leu Asp Glu Gly 40 Thr Gly 55	Gly 25 Asp	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val 60	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr	
Met Gln Gln Val Pro Ile Ser Val Ser 35 Leu Lys Phe 50	Leu Val 20 Gly Glu Ile Cys	Glu I Gly C Thr T	Leu Asp Glu Gly 40 Thr Gly 55	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln	Val Thr Pro Cys 75	Asn Tyr Val 60 Phe	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr Thr Pro 80	
Met Gln Gln 1 Val Pro Ile Ser Val Ser 35 Leu Lys Phe 50 Leu Val Thr 65	Leu Val 20 Gly Glu Ile Cys Thr Phe	Glu I Gly C Thr T	Leu Asp Glu Gly 40 Thr Gly 55 Tyr Gly Asp Phe	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln Lys 90	Val Thr Pro Cys 75 Ser	Asn Tyr Val 60 Phe	Gly 45 Pro Ser	His 30 Lys Trp Arg	Lys Leu Pro Tyr Glu 95	Phe Thr Thr Pro 80 Gly	
Met Gln Gln Val Pro Ile Ser Val Ser 35 Leu Lys Phe 50 Leu Val Thr 65 Asp His Met	Leu Val 20 Gly Glu Ile Cys Thr Phe Lys Gln 85 Glu Arg 100 Glu Val	Glu I Gly C Thr 7 Ser 7 70 His A	Leu Asp Glu Gly 40 Thr Gly 55 Tyr Gly Asp Phe	Gly 25 Asp Lys Val Phe	Asp Ala Leu Gln Lys 90 Lys	Val Thr Pro Cys 75 Ser Asp	Asn Tyr Val 60 Phe Ala Asp	Gly Gly 45 Pro Ser Met	His 30 Lys Trp Arg Pro	Lys Leu Pro Tyr Glu 95 Tyr	Phe Thr Thr Pro 80 Gly Lys	

145		Tyr Asn Ser 150	His Asn Va	l Tyr Ile Me	t Ala Asp 160
Lys Gln Lys	Asn Gly 1 165	Ile Lys Val	Asn Phe Ly	s Ile Arg Hi	s Asn Ile 175
	Ser Val 0 180	Gln Leu Ala	Asp His Ty: 185	r Gln Gln Ası 19	
Ile Gly Asp 195	Gly Pro V	Val Leu Leu 200	_	n His Tyr Le 205	u Ser Thr
Gln Ser Ala 210	Leu Ser I	Lys Asp Pro 215	Asn Glu Ly	s Arg Asp His 220	s Met Val
Leu Leu Glu 225		Thr Ala Ala 230	Gly Ile Th	r His Gly Med 5	t Asp Glu 240
Leu Tyr Lys		•			
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tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	336
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	384
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	432
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	480
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
cag tet gee etg tet aaa gat eee aac gaa aag aga gae eac atg gte Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	

35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 37

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

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<221> CDS

<222> (1)..(732)

<400> 37

atg gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg

Met Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1 5 10 15

_					gaa Glu				_							96
	_	-		-	ggt Gly	_		_	_				_			144
_				-	acc Thr			_			_					192
_	_				tct Ser 70				_	_			_	Tyr		240
-		_	_	_	cat His	_					_	_				288
					acc Thr											336
	_	_	_	_	aag Lys		_		_		_			_		384
	-	_			gac Asp		-	_	_							432
					tat Tyr 150											480
_		_			atc Ile	_	_			_		_				528
	gat	gga	tcc	ata	caq	cta	acc	gac	cat	tat	C 2 2	cad	aac	act	cca	576
	Asp	Gly			Gln	-	_	_				_			Pro	
	ggc	gac	Ser 180 ggc	Val	-	Leu	Ala	Asp 185 cca	His gac	Tyr aac	Gln cat	Gln	Asn 190 ctg	Thr	acc	624
Ile cag	ggc Gly tct	gac Asp 195 gcc	Ser 180 ggc Gly ctg	Val cct Pro	Gln	Leu ctc Leu gat	Ala ctc Leu 200	Asp 185 cca Pro	His gac Asp	Tyr aac Asn aag	Gln cat His	Gln tac Tyr 205 gac	Asn 190 ctg Leu cac	Thr tcc Ser	acc Thr	624 672

ctg tac aag tga Leu Tyr Lys

<210> 38

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Glu(GAA)5GFP

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Met Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

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Leu Tyr Lys

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	528
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	576
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235 230 235 240	720
ctg tac aag tga Leu Tyr Lys	732
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Lys Leu Glu 145	Tyr Asn	Tyr Asn 150	Ser His	Asn Val 155	Tyr Ile	Met Ala	Asp 160
Lys Gln Lys	Asn Gly 165	Ile Lys	Val Asn	Phe Lys 170	Ile Arg	His Asn 175	Ile
Glu Asp Gly	Ser Val 180	Gln Leu	Ala Asp 185	His Tyr	Gln Gln	Asn Thr 190	Pro
Ile Gly Asp 195		Val Leu	Leu Pro 200	Asp Asn	His Tyr 205	Leu Ser	Thr
Gln Ser Ala 210	Leu Ser	Lys Asp 215	Pro Asn	Glu Lys	Arg Asp 220	His Met	Val
Leu Leu Glu 225	Phe Val	Thr Ala 230	Ala Gly	Ile Thr 235	His Gly	Met Asp	Glu 240
Leu Tyr Lys							
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		E Artific	cial Sequ	ience: G	ly(GGA) 50	GFP	
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gac cat atg Asp His Met		_			_	_	_	_				288
tat gtg cag Tyr Val Gln						_	_				-	336
acc cgc gct Thr Arg Ala 115												384
gag ctg aag Glu Leu Lys 130		_	e Lys	_								432
aag ctg gaa Lys Leu Glu 145									_	-	_	480
aag caa aag Lys Gln Lys												528
gag gat gga Glu Asp Gly		_		-				_				576
atc ggc gac Ile Gly Asp 195		-			_				_			624
cag tct gcc Gln Ser Ala 210			p Pro									672
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ctg tac aag Leu Tyr Lys	tga											732
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Val Pro Ile	Leu Val	Glu Le	u Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	

20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

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Leu Tyr Lys

<210> 43

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Gly(GGC)5GFP

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					ggt Gly											144
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					tct Ser 70											240
					cat His											288
					acc Thr											336
					aag Lys											384
					gac Asp											432
					tat Tyr 150											480
					atc Ile											528
					cag Gln											576
_					gtg Val											624
					aaa Lys											672
ctg	ctg	gag	ttt	gtg	acc	gct	gct	aaa	atc	aca	cat	ggc	atg	gac	gag	720

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 235 240 732 ctg tac aag tga Leu Tyr Lys <210> 44 <211> 243 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence: Gly(GGC)5GFP <400> 44 Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

220

215

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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

235

145	.Tyr Asn	Tyr A:	sn Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
aag caa aag Lys Gln Lys												528
gag gat gga Glu Asp Gly												576
atc ggc gac Ile Gly Asp 195					_				_			624
cag tct gcc Gln Ser Ala 210	_	Lys A			_	_	_	_		_	_	672
ctg ctg gag Leu Leu Glu 225												720
ctg tac aag Leu Tyr Lys	tga											732
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Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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Leu	Tyr	Lys														
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	l> CI		(732)	ı												
)> 47															
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					gaa Glu											96
	_	-			ggt Gly	-		_	_				_			144
					acc Thr											192
ctg	gtc	act	acc	ttc	tct	tat	ggc	gtg	cag	tgc	ttt	tcc	aga	tac	cca	240

Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
							ttt Phe									288
							ttt Phe									336
							gaa Glu 120									384
							aag Lys									432
							tcc Ser									480
							gtc Val									528
				-	_	_	gcc Ala	_				_				576
							ctc Leu 200									624
							ccc Pro									672
							gct Ala									720
-	tac Tyr		tga													732
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1 5 10 15

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

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Leu Tyr Lys

<210> 49

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<212> DNA

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<220>

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	_				_	acc Thr			_			-					192
						tct Ser 70											240
						cat His											288
			_		_	acc Thr					_	-				_	336
						aag Lys										atc Ile	384
						gac Asp											432
						tat Tyr 150											480
	_		_			atc Ile	-	-			-		_				528
	Glu	Asp	Gly	Ser 180	Val	cag Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	576
	Ile	Gly	Asp 195	Gly	Pro	gtg Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	624
	_		_	_		aaa Lvs	_			_	_	_	_		_	_	672

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val

210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 240

ctg tac aag tga 732 Leu Tyr Lys

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<211> 243

<212> PRT

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<220>

<223> Description of Artificial Sequence: His(CAC)5GFP

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235 Leu Tyr Lys <210> 51 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: His(CAT)5GFP <220> <221> CDS <222> (1)..(732) <400> 51 atg cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg Met His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 etg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110 acc ege get gaa gte aag tte gaa ggt gae acc etg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His

	13	5	140										
			Tyr Ile Met Ala Asp	80									
			atc aga cac aac att 5 Ile Arg His Asn Ile 175	28									
	Val Gln Le		caa cag aac act cca 5 Gln Gln Asn Thr Pro 190	76									
			cat tac ctg tcc acc 6 His Tyr Leu Ser Thr 205	24									
		p Pro Asn Glu Lys	aga gac cac atg gtc 6 Arg Asp His Met Val 220	72									
			cat ggc atg gac gag 7 His Gly Met Asp Glu 240	20									
ctg tac aag tga Leu Tyr Lys			7	32									
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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Leu Tyr Lys
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
Val Pro Ile Leu Val Glu-Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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50 55 60

ctg g Leu V 65																240
gac c Asp H		_	_	_		_			-	_	-	_				288
tat g Tyr V			_	_						_	-				-	336
acc c Thr A																384
gag c Glu I 1							_		_							432
aag o Lys I 145	_	_											_	_	_	480
aag c Lys G		_				_	_			_		_				528
gag g Glu A	-				_	_	_	_				_				576
atc g Ile G	3ly	-							_				_			624
cag t Gln S			_			_			_	-	-	-		_	-	672
ctg c Leu I 225																720
ctg t Leu T		_	tga													732

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<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ile(ATA)5GFP

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

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205

200

					aaa Lys	-			_	_	_	_		_	_	672
					acc Thr 230											720
	tac Tyr	-	tga													732
<210> 56 <211> 243 <212> PRT <213> Artificial Sequence																
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	0> 50 Ile		Ile	Ile	Ile	Ser	Lvs	Glv	Glu	Glu	Len	Phe	Thr	Glv	Val	
1				5		201	2,0	CLY	10	oru	Dea	1110		15	Val	
Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205														
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220														
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240														
Leu Tyr Lys	•													
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	96													
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	144													
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	192													
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	240													
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	288													
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	336													
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	384													

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140													
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160													
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175													
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190													
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205													
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220													
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240													
ctg tac aag tga Leu Tyr Lys	732												
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                            120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                     170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
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Leu Tyr Lys
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                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
                             40
                                                 45
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ctg a Leu I																192
ctg g Leu V 65																240
gac c Asp H		_	_	_		-			_	-	-	_				288
tat g Tyr V	-	_		_						_	_				_	336
acc c																384
gag c Glu I 1		_			_		_									432
aag c Lys I 145													_	_	-	480
aag c Lys G						-				-		_				528
gag g Glu A					_	_	_	_				_				576
atc g Ile G	-	_							_				_			624
cag t Gln S																672
ctg c Leu I 225																720
ctg t Leu T			tga													732
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 61

<211> 732

<212> DNA

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					gtg Val											624
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					acc Thr 230											720
_	tac Tyr	aag Lys	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
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Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	•
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	

Giu	Asp	GIY	180	vai	GIII	ьeu	AIA	185	пір	TÀT	GIII	GIII	190	Inr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
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Leu	Tyr	Lys														
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					gaa Glu											96
					ggt Gly											144
					acc Thr											192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
					cat His											288
					acc Thr											336

acc cgc gct Thr Arg Ala 115	Glu Val						
gag ctg aag Glu Leu Lys 130							
aag ctg gaa Lys Leu Glu 145					Tyr Ile		
aag caa aag Lys Gln Lys		_	_	_	_		Ile
gag gat gga Glu Asp Gly				His Tyr			
atc ggc gac Ile Gly Asp 195	Gly Pro			_		_	
cag tot goo Gln Ser Ala 210	_	_				_	_
ctg ctg gag Leu Leu Glu 225		_			His Gly		
ctg tac aag Leu Tyr Lys							732
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Ser Val Ser		Gly Glu	Gly Asp 40	Ala Thr	Tyr Gly 45	Lys Leu	Thr
Leu Lys Phe							

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 65
                     70
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Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                 105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                    150
                                         155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195
                                                 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                    230
                                         235
Leu Tyr Lys
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                                                          15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
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					acc Thr											192
ctg Leu 65	gtc Val	act Thr	acc Thr	ttc Phe	tct Ser 70	tat Tyr	ggc Gly	gtg Val	cag Gln	tgc Cys 75	ttt Phe	tcc Ser	aga Arg	tac Tyr	cca Pro 80	240
					cat His											288
tat Tyr	gtg Val	cag Gln	gag Glu 100	aga Arg	acc Thr	atc Ile	ttt Phe	ttc Phe 105	aaa Lys	gat Asp	gac Asp	gly ggg	aac Asn 110	tac Tyr	aag Lys	336
					aag Lys											384
gag Glu	ctg Leu 130	aag Lys	ggc Gly	att Ile	gac Asp	ttt Phe 135	aag Lys	gag Glu	gat Asp	gga Gly	aac Asn 140	att Ile	ctc Leu	ggc Gly	cac His	432
					tat Tyr 150											480
					atc Ile											528
					cag Gln											576
					gtg Val											624
					aaa Lys											672
ctg Leu 225	ctg Leu	gag Glu	ttt Phe	gtg Val	acc Thr 230	gct Ala	gct Ala	gly ggg	atc Ile	aca Thr 235	cat His	ggc Gly	atg Met	gac Asp	gag Glu 240	720
_	tac Tyr	aag Lys	tga													732

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Leu(CTT)5GFP

<400> 66

Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 67

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<211> 732
<212> DNA
<213> Artificial Sequence
<220>
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<220>
<221> CDS
<222> (1)..(732)
<400> 67
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Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                                          15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
                                     90
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac
                                                                   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                                        155
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arq His Asn Ile
                165
                                    170
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca
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Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
		gac Asp 195							_				_			624
		gcc Ala														672
		gag Glu														720
_	tac Tyr	aag Lys	tga													732
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	0> 61 Leu	B Leu	Leu	Leu 5	Leu	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	
Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
Leu 65	Val	Thr	Thr	Phe	Ser 70	Tyr	Gly	Val	Gln	Cys 75	Phe	Ser	Arg	Tyr	Pro 80	
Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	
Leu Tyr Lys	
<210> 69 <211> 732	
<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Leu(TTG)5GFP	
<220> <221> CDS <222> (1)(732)	
<400> 69 atg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
atg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15	
atg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val	
atg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg 48 Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe	
atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr	
atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1 5 10 15 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr	
Atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 1	

Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
					aag Lys											384
	-	_			gac Asp		_		-							432
_	_	-			tat Tyr 150								_	-	_	480
_		_			atc Ile	_	_			_		_				528
					cag Gln											576
		_			gtg Val				_				_			624
					aaa Lys	_			_	_	_	_		_	_	672
	-				acc Thr 230	_	_						_	_		720
_	tac Tyr	aag Lys	tga													732
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)> 7(Len		I.em	I.em	Leu	Ser	Lve	Glv	Glu	Glu	T.e.11	Dhe	Thr	Glv	Val	
1	Leu	D GU	Leu	5	LCU	DGI	шys	U.Y	10	Jiu	шcu	THE	****	15	val	
Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser	Val	Ser 35	Gly	Glu	Gly	Glu	Gly 40	Asp	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
                          55
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                     70
                                          75
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                 105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                            120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                    150
                                         155
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                        215
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
                                        235
                                                             240
Leu Tyr Lys
<210> 71
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Lys(AAA)5GFP
<220>
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<222> (1)..(732)
<400> 71
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                                                                   48
Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                                          15
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
	_	_		_		_		-	_		tac Tyr					144
_				_				_			gtg Val 60					192
_	_								_	_	ttt Phe		_			240
_		_	_	_		_			_	_	gcc Ala	_				288
											gac Asp					336
	_	_	_	_	_		_	-			ctg Leu					384
											aac Asn 140					432
											tac Tyr					480
											atc Ile					528
	_				_	_	_	-			caa Gln	_				576
		_							-		cat His		_			624
											aga Arg 220					672
											cat His					720
	tac Tyr		tga					٠								732

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<210> 72
<211> 243
<212> PRT
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Lys(AAA)5GFP

<400> 72

Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

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<210> 73
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Lys(AAG)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 73
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Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                                     10
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
                                                                   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
                         55
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                                         75
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                            120
                                                 125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac
                                                                   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                                                             160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
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GIu		gga Gly														576
		gac Asp 195							_				_			624
		gcc Ala														672
	Leu	gag Glu														720
_	tac Tyr	aag Lys	tga													732
<21 <21	0> 74 1> 24 2> Pl 3> A	13	icia]	L Sec	quenc	ce										
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	0> 74 Lys	l Lys	Lys	Lys 5	Lys	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
Met 1	Lys			5			_	_	10					15		
Met 1 Val	Lys Pro	Lys	Leu 20	5 Val	Glu	Leu	Asp	Gly 25	10 Asp	Val	Asn	Gly	His 30	15 Lys	Phe	
Met 1 Val Ser	Lys Pro Val	Lys Ile Ser	Leu 20 Gly	5 Val Glu	Glu Gly	Leu Glu	Asp Gly 40	Gly 25 Asp	10 Asp Ala	Val Thr	Asn Tyr	Gly Gly 45	His 30 Lys	Lys	Phe Thr	
Met 1 Val Ser Leu	Pro Val Lys 50	Lys Ile Ser 35	Leu 20 Gly Ile	5 Val Glu Cys	Glu Gly Thr	Leu Glu Thr 55	Asp Gly 40 Gly	Gly 25 Asp Lys	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val 60	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu	Phe Thr	
Met 1 Val Ser Leu 65	Pro Val Lys 50 Val	Lys Ile Ser 35 Phe	Leu 20 Gly Ile Thr	5 Val Glu Cys Phe	Glu Gly Thr Ser 70	Leu Glu Thr 55 Tyr	Asp Gly 40 Gly Gly	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln	Val Thr Pro Cys 75	Asn Tyr Val 60 Phe	Gly Gly 45 Pro Ser	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr Thr Pro 80	
Met 1 Val Ser Leu 65 Asp	Pro Val Lys 50 Val	Lys Ile Ser 35 Phe Thr	Leu 20 Gly Ile Thr	Val Glu Cys Phe Gln 85	Glu Gly Thr Ser 70	Leu Glu Thr 55 Tyr	Asp Gly 40 Gly Gly Phe	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln Lys 90	Val Thr Pro Cys 75 Ser	Asn Tyr Val 60 Phe Ala	Gly 45 Pro Ser	His 30 Lys Trp Arg	Leur Pro Tyr Glu	Phe Thr Thr Pro 80 Gly	
Met 1 Val Ser Leu 65 Asp	Pro Val Lys 50 Val His	Lys Ile Ser 35 Phe Thr	Leu 20 Gly Ile Thr Lys Glu 100	Val Glu Cys Phe Gln 85 Arg	Glu Gly Thr Ser 70 His	Leu Glu Thr 55 Tyr Asp	Asp Gly 40 Gly Gly Phe	Gly 25 Asp Lys Val Phe 105	Asp Ala Leu Gln Lys 90 Lys	Val Thr Pro Cys 75 Ser	Asn Tyr Val 60 Phe Ala Asp	Gly 45 Pro Ser Met	His 30 Lys Trp Arg Pro	Lys Leu Pro Tyr Glu 95 Tyr	Phe Thr Thr Pro 80 Gly Lys	

145	Tyr Asn	Tyr Asn 150	Ser His	Asn Val 155	Tyr Ile	Met Al	a Asp 160	
Lys Gln Lys	Asn Gly	Ile Lys	Val Asn	Phe Lys 170	Ile Arg	His As		
Glu Asp Gly	Ser Val (Gln Leu	Ala Asp 185	His Tyr	Gln Gln	Asn Th	r Pro	
Ile Gly Asp 195	_	Val Leu	Leu Pro 200	Asp Asn	His Tyr 205	Leu Se	r Thr	
Gln Ser Ala 210	Leu Ser	Lys Asp 215	Pro Asn	Glu Lys	Arg Asp 220	His Me	t Val	
Leu Leu Glu 225		Thr Ala 230	Ala Gly	Ile Thr 235	His Gly	Met As	o Glu 240	
Leu Tyr Lys								
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<220> <223> Descr	iption of	Artific	ial Seq	uence: Pl	ne (TTT) 50	GFP		
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<221> CDS <222> (1)	ttt ttt						y Val	18
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<221> CDS <222> (1) <400> 75 atg ttt ttt Met Phe Phe 1 gtc cca att Val Pro Ile tct gtc agc Ser Val Ser	ttt ttt phe p	Phe Ser gaa ctg Glu Leu ggt gaa Gly Glu acc act	gat ggc Asp Gly 25 ggt gat Gly Asp 40	Glu Glu 10 gat gtg Asp Val gcc aca Ala Thr ctc cct	Leu Phe aat ggg Asn Gly tac gga Tyr Gly 45 gtg cca	Thr Gl 1 cac aa His Ly 30 aag ct Lys Le tgg cc	y Val 5 a ttt 9 s Phe c acc 1 1 Thr	96
<221> CDS <222> (1) <400> 75 atg ttt ttt Met Phe Phe 1 gtc cca att Val Pro Ile tct gtc agc Ser Val Ser 35 ctg aaa ttc Leu Lys Phe	ttt ttt phe p	Phe Ser gaa ctg Glu Leu ggt gaa Gly Glu acc act Thr Thr 55	Lys Gly gat ggc Asp Gly 25 ggt gat Gly Asp 40 gga aag Gly Lys ggc gtg	Glu Glu 10 gat gtg Asp Val gcc aca Ala Thr ctc cct Leu Pro cag tgc	Leu Phe aat ggg Asn Gly tac gga Tyr Gly 45 gtg cca Val Pro 60 ttt tcc	Thr Gl 1 cac aa His Ly 30 aag ct Lys Le tgg cc Trp Pr aga ta	y Val a ttt 9 s Phe c acc 1 i Thr a aca 1 o Thr	96

									,					,,,		
					acc Thr											336
					aag Lys											384
					gac Asp		_	_	_							432
					tat Tyr 150								_	_	-	480
_		_			atc Ile	_	_			_		_				528
					cag Gln											576
					gtg Val											624
					aaa Lys											672
					acc Thr 230											720
_	tac Tyr	aag Lys	tga													732
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Val	Pro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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                             40
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                                185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
                                                205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                                        235
Leu Tyr Lys
<210> 77
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			tct Ser 70						240
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			acc Thr						336
			aag Lys						384
			gac Asp						432
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			atc Ile						528
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35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

155

160

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150

Lys Gln Lys	aat ggc Asn Gly 165	Ile Lys								528
gag gat gga Glu Asp Gly			Ala A							576
atc ggc gac Ile Gly Asp 195				_			_			624
cag tct gcc Gln Ser Ala 210						Asp				672
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ctg tac aag Leu Tyr Lys	_									732
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175	
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190	
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	
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		aac tcc cac Asn Ser His			
		aag gtc aac Lys Val Asn	_	_	
		ctg gcc gac Leu Ala Asp 185			
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195
                            200
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				cat His											288
				acc Thr											336
				aag Lys											384
_	_	_		gac Asp		_		_							432
_	_	_		tat Tyr 150								_	_	_	480
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			_	cag Gln	_	-	_				_				576
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Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	

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215

220

210

130

Lys Leu 145	gaa Glu														480
aag caa Lys Gln	_				_	_			_						528
gag gat Glu Asp				_	_	_	_				_				576
atc ggc Ile Gly															624
cag tct Gln Ser 210	Ala				_			_	_	_	_		_	-	672
ctg ctg Leu Leu 225															720
ctg tac Leu Tyr	_	tga													732
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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
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Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                                 25
tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace
                                                                   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
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ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
                         55
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					_		_	_	_	gga Gly						432
										gtg Val 155			_	_	_	480
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								-		tat Tyr		-				576
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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cag tot goo otg tot aaa gat ooc aac qaa aaq aqa qac cac atq qto

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 ctg tac aag tga 732 Leu Tyr Lys <210> 90 <211> 243 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Ser (AGT) 5GFP Met Ser Ser Ser Ser Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys <210> 91 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Ser (TCA) 5GFP <220> <221> CDS <222> (1)..(732) <400> 91 atg tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg Met Ser Ser Ser Ser Ser Lys Gly Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 ctg gtc act acc ttc tct tat qqc qtq caq tqc ttt tcc aqa tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys acc ege get gaa gte aag tte gaa ggt gae acc etg gtg aat aga ate 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 120

200

205

195

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac

Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
														gcc Ala		480
		_				_	_			_		_		aac Asn 175		528
														act Thr		576
		_							_				_	tcc Ser		624
			_			_			-	_	_	_		atg Met	-	672
_	_					-	-						_	gac Asp		720
_	tac Tyr	aag Lys	tga													732
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	0> 92 Ser	2 Ser	Ser	Ser	Ser	Ser	Lvs	C1				_,	The	Glv	Val	
				5			-,,	GIY	Glu 10	Glu	Leu	Phe	1111	15		
Val	Pro	Ile	Leu 20				_	_	10					_		
			20	Val	Glu	Leu	Asp	Gly 25	10 Asp	Val	Asn	Gly	His 30	15	Phe	
Ser	Val	Ser 35	20 Gly	Val Glu	Glu Gly	Leu Glu	Asp Gly 40	Gly 25 Asp	10 Asp Ala	Val Thr	Asn Tyr	Gly Gly 45	His 30 Lys	15 Lys	Phe Thr	
Ser Leu	Val Lys 50	Ser 35 Phe	20 Gly Ile	Val Glu Cys	Glu Gly Thr	Leu Glu Thr 55	Asp Gly 40	Gly 25 Asp	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val 60	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu	Phe Thr	

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 185 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr. 200 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 235 Leu Tyr Lys <210> 93 <211> 732 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Ser(TCC) 5GFP <220> <221> CDS <222> (1)..(732) <400> 93 atg tee tee tee tee age aag gge gag gaa etg tte act gge gtg 48 Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val 5 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca

Leu	Lys 50	Phe	Ile	Cys	Thr	Thr 55	Gly	Lys	Leu	Pro	Val 60	Pro	Trp	Pro	Thr	
														tac Tyr		240
														gag Glu 95		288
		_		_						_	_			tac Tyr	_	336
	_			_	_		_		_		-			aga Arg		384
														ggc Gly		432
_	_	-											_	gcc Ala	_	480
										_		-		aac Asn 175		528
				-	_		-	_				_		act Thr		576
		-							-				_	tcc Ser		624
														atg Met		672
														gac Asp		720
	tac Tyr	aag Lys	tga													732
<210)> 94	Į.														

<211> 243

<212> PRT <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ser(TCC)5GFP

<400> 94

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 95

<211> 732

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artific	cial Sequence: Ser(TCG)5GFP
<220> <221> CDS <222> (1)(732)	
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	gat ggc gat gtg aat ggg cac aaa ttt 96 Asp Gly Asp Val Asn Gly His Lys Phe 25 30
	ggt gat gcc aca tac gga aag ctc acc 144 Gly Asp Ala Thr Tyr Gly Lys Leu Thr 40 45
	gga aag ctc cct gtg cca tgg cca aca 192 Gly Lys Leu Pro Val Pro Trp Pro Thr 60
	ggc gtg cag tgc ttt tcc aga tac cca 240 Gly Val Gln Cys Phe Ser Arg Tyr Pro 75 80
	ttt ttc aag agc gcc atg ccc gag ggc 288 Phe Phe Lys Ser Ala Met Pro Glu Gly 90 95
	ttt ttc aaa gat gac ggg aac tac aag 336 Phe Phe Lys Asp Asp Gly Asn Tyr Lys 105 110
	gaa ggt gac acc ctg gtg aat aga atc 384 Glu Gly Asp Thr Leu Val Asn Arg Ile 120 125
	aag gag gat gga aac att ctc ggc cac 432 Lys Glu Asp Gly Asn Ile Leu Gly His 140
	tcc cac aat gtg tac atc atg gcc gac 480 Ser His Asn Val Tyr Ile Met Ala Asp 155 160
	gtc aac ttc aag atc aga cac aac att 528 Val Asn Phe Lys Ile Arg His Asn Ile 170 175
	gcc gac cat tat caa cag aac act cca 576 Ala Asp His Tyr Gln Gln Asn Thr Pro 185 190
	ctc cca gac aac cat tac ctg tcc acc 624 Leu Pro Asp Asn His Tyr Leu Ser Thr

195 200 205 cag tot goo etg tot aaa gat eec aac gaa aag aga gac cac atg gto Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 . 230 235

ctg tac aag tga 732 Leu Tyr Lys

<210> 96

<211> 243 <212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Ser(TCG)5GFP

<400> 96

Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 70

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 135

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	
Leu Tyr Lys	
<210> 97 <211> 732 <212> DNA <213> Artificial Sequence	
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30	5
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	44
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 19 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	92
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 24 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	40
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 28 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	88
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 33 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	36
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 38 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile	84

115	120		125
gag ctg aag ggc at Glu Leu Lys Gly Il 130			
aag ctg gaa tac aa Lys Leu Glu Tyr As 145			
aag caa aag aat gg Lys Gln Lys Asn Gl 16	y Ile Lys Val		-
gag gat gga tcc gt Glu Asp Gly Ser Va 180		•	_
atc ggc gac ggc co Ile Gly Asp Gly Pr 195		•	3
cag tot god otg to Gln Ser Ala Leu Se 210	-		
ctg ctg gag ttt gt Leu Leu Glu Phe Va 225			
ctg tac aag tga Leu Tyr Lys			732
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Val Pro Ile Leu Va 20	l Glu Leu Asp	Gly Asp Val Asn 25	Gly His Lys Phe
Ser Val Ser Gly Gl 35	u Gly Glu Gly 40	Asp Ala Thr Tyr	Gly Lys Leu Thr 45
Leu Lys Phe Ile Cy 50	s Thr Thr Gly 55	Lys Leu Pro Val 60	Pro Trp Pro Thr
Leu Val Thr Thr Ph	e Ser Tyr Gly 70	Val Gln Cys Phe 75	Ser Arg Tyr Pro 80

Asp	His	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
Tyr	Val	Gln	Glu 100	Arg	Thr	Ile	Phe	Phe 105	Lys	Asp	Asp	Gly	Asn 110	Tyr	Lys	
Thr	Arg	Ala 115	Glu	Val	Lys	Phe	Glu 120	Gly	Asp	Thr	Leu	Val 125	Asn	Arg	Ile	
Glu	Leu 130	Lys	Gly	Ile	Asp	Phe 135	Lys	Glu	Asp	Gly	Asn 140	Ile	Leu	Gly	His	
Lys 145	Leu	Glu	Tyr	Asn	Tyr 150	Asn	Ser	His	Asn	Val 155	Tyr	Ile	Met	Ala	Asp 160	
Lys	Gln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val	Leu	Leu 200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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	0> L> CI 2> (1	-	(732)	ı												
atg	0> 99 aca Thr	aca														48
	cca Pro															96
	gtc Val															144

-				-	acc Thr			_							192
_					tct Ser 70			-	-	_			_		240
					cat His										288
			-	-	acc Thr					-	_			_	336
					aag Lys										384
	_	_			gac Asp		_		_						432
					tat Tyr 150										480
		-			atc Ile	_	_			_		_			528
					cag Gln										57 <u>6</u>
		_			gtg Val				_				_		624
					aaa Lys										672
					acc Thr 230										720
	tac Tyr	aag Lys	tga												732
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr (ACA) 5GFP

<400> 100

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 55 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

<210> 101

<211> 732

<212> DNA

<213> Artificial Sequence <220> <223> Description of Artificial Sequence: Thr(ACC)5GFP <220> <221> CDS <222> (1)..(732) <400> 101 atg acc acc acc acc agc aag ggc gag gaa ctg ttc act ggc gtg Met Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 150 155 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 170 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205	624
cag tot goo otg tot aaa gat ooc aac gaa aag aga gac oac atg gto Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220	672
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240	720
ctg tac aag tga Leu Tyr Lys	732
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<220> <223> Description of Artificial Sequence: Thr(ACC)5GFP	
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45	
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 50 55 60	
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80	
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95	
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 110	
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125	
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140	
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160	
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile	

Glu	Asp	Gly	Ser 180	Val	Gln	Leu	Ala	Asp 185	His	Tyr	Gln	Gln	Asn 190	Thr	Pro	
Ile	Gly	Asp 195	Gly	Pro	Val		Leu .200	Pro	Asp	Asn	His	Tyr 205	Leu	Ser	Thr	
Gln	Ser 210	Ala	Leu	Ser	Lys	Asp 215	Pro	Asn	Glu	Lys	Arg 220	Asp	His	Met	Val	
Leu 225	Leu	Glu	Phe	Val	Thr 230	Ala	Ala	Gly	Ile	Thr 235	His	Gly	Met	Asp	Glu 240	
Leu	Tyr	Lys														
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	L> CI	os L)	(732))												
)> 10															
					acg Thr											48
					gaa Glu											96
					ggt Gly											144
					acc Thr											192
					tct Ser 70											240
					cat His											288
					acc Thr											336

acc cgc gct ga Thr Arg Ala Gl 115		_		_		_	
gag ctg aag gg Glu Leu Lys Gl 130							
aag ctg gaa ta Lys Leu Glu Ty 145					_	Ala A	•
aag caa aag aa Lys Gln Lys As							
gag gat gga to Glu Asp Gly Se 18	r Val Gln	Leu Ala	_		_		
atc ggc gac gg Ile Gly Asp Gl 195			_		_		
cag tct gcc ct Gln Ser Ala Le 210	-	_	-		_		
ctg ctg gag tt Leu Leu Glu Ph 225						Asp G	
ctg tac aag tg Leu Tyr Lys	a						732
<210> 104 <211> 243 <212> PRT <213> Artifici	al Sequenc	ce					
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Val Pro Ile Le 2		Leu Asp	Gly Asp 25	Val Asn	Gly His	Lys P	Phe
Ser Val Ser Gl 35	y Glu Gly	Glu Gly 40	Asp Ala	Thr Tyr	Gly Lys 45	Leu T	Chr
Leu Lys Phe Il 50	e Cys Thr	Thr Gly :	Lys Leu	Pro Val 60	Pro Trp	Pro T	Thr

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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                    150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210
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Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
                    230
Leu Tyr Lys
<210> 105
<211> 732
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Thr(ACT)5GFP
<220>
<221> CDS
<222> (1)..(732)
<400> 105
atg act act act act agc aag ggc gag gaa ctg ttc act ggc gtg
Met Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20
                                 25
```

							ggt Gly 40								144
							gga Gly								192
							ggc Gly								240
				_		_	ttt Phe	_	_	_	_				288
							ttt Phe		-	_				_	336
							gaa Glu 120								384
							aag Lys								432
_	_	_					tcc Ser					_	_	_	480
						_	gtc Val		_		-				528
					_		gcc Ala				_				576
		_					ctc Leu 200	_				_			624
_		_	_			_	ccc Pro	_	_	_	_		_	-	672
							gct Ala								720
_	tac Tyr	aag Lys	tga												732

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<210> 106
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<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thr(ACT)5GFP

<400> 106

Met Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

1 5 10 15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

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<210> 107
<211> 732
<212> DNA
<213> Artificial Sequence
<220>
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<220>
<221> CDS
<222> (1)..(732)
<400> 107
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gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt
                                                                   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50
                         55
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca
                                                                   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65
                     70
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc
                                                                   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag
                                                                   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                                105
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc
                                                                   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                            120
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac
                                                                   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac
                                                                   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145
                                                             160
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165
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Glu						ctg Leu										576
						ctc Leu										624
						gat Asp 215										672
						gct Ala										720
-	tac Tyr	aag Lys	tga													732
<213 <213	0> 10 L> 24 2> PI B> Ai	13 RT	icial	L Sec	quenc	ce										
<220 <223		escri	iptio	on of	E Art	cific	cial	Sequ	ience	e: T1	T) q:	GG) 50	SFP			
-400)> 10	nΩ														
			Trp	Trp 5	Trp	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	Gly 15	Val	
Met 1	Trp	Trp		5		Ser Leu	_	_	10					15		
Met 1 Val	Trp Pro	Trp	Leu 20	5 Val	Glu		Asp	Gly 25	10 Asp	Val	Asn	Gly	His 30	15 Lys	Phe	
Met 1 Val Ser	Trp Pro Val	Trp Ile Ser 35	Leu 20 Gly	5 Val Glu	Glu Gly	Leu	Asp Gly 40	Gly 25 Asp	10 Asp Ala	Val Thr	Asn Tyr	Gly Gly 45	His 30 Lys	15 Lys Leu	Phe Thr	
Met 1 Val Ser	Trp Pro Val Lys 50	Trp Ile Ser 35 Phe	Leu 20 Gly Ile	5 Val Glu Cys	Glu Gly Thr	Leu Glu Thr	Asp Gly 40	Gly 25 Asp Lys	10 Asp Ala Leu	Val Thr Pro	Asn Tyr Val 60	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr	
Met 1 Val Ser Leu 65	Trp Pro Val Lys 50 Val	Trp Ile Ser 35 Phe Thr	Leu 20 Gly Ile	5 Val Glu Cys Phe	Glu Gly Thr Ser 70	Leu Glu Thr 55	Asp Gly 40 Gly Gly	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln	Val Thr Pro Cys 75	Asn Tyr Val 60 Phe	Gly Gly 45 Pro	His 30 Lys Trp	15 Lys Leu Pro	Phe Thr Thr Pro 80	
Met 1 Val Ser Leu 65 Asp	Trp Pro Val Lys 50 Val His	Trp Ile Ser 35 Phe Thr	Leu 20 Gly Ile Thr	Val Glu Cys Phe Gln 85	Glu Gly Thr Ser 70	Leu Glu Thr 55 Tyr	Asp Gly 40 Gly Gly Phe	Gly 25 Asp Lys Val	10 Asp Ala Leu Gln Lys 90	Val Thr Pro Cys 75 Ser	Asn Tyr Val 60 Phe	Gly Gly 45 Pro Ser	His 30 Lys Trp Arg	Lys Leu Pro Tyr Glu 95	Phe Thr Thr Pro 80 Gly	
Met 1 Val Ser Leu 65 Asp	Trp Pro Val Lys 50 Val His	Trp Ile Ser 35 Phe Thr Met	Leu 20 Gly Ile Thr Lys Glu 100	Val Glu Cys Phe Gln 85 Arg	Glu Gly Thr Ser 70 His	Leu Glu Thr 55 Tyr	Asp Gly 40 Gly Gly Phe	Gly 25 Asp Lys Val Phe 105	Asp Ala Leu Gln Lys 90 Lys	Val Thr Pro Cys 75 Ser Asp	Asn Tyr Val 60 Phe Ala Asp	Gly Gly 45 Pro Ser Met	His 30 Lys Trp Arg Pro	Lys Leu Pro Tyr Glu 95 Tyr	Phe Thr Thr Pro 80 Gly Lys	
Met 1 Val Ser Leu 65 Asp Tyr	Trp Pro Val Lys 50 Val His Val	Trp Ile Ser 35 Phe Thr Met Gln Ala 115	Leu 20 Gly Ile Thr Lys Glu 100 Glu	Val Glu Cys Phe Gln 85 Arg Val	Glu Gly Thr Ser 70 His Thr	Leu Glu Thr 55 Tyr Asp	Asp Gly 40 Gly Gly Phe Phe Glu 120	Gly 25 Asp Lys Val Phe 105 Gly	Asp Ala Leu Gln Lys 90 Lys Asp	Val Thr Pro Cys 75 Ser Asp	Asn Tyr Val 60 Phe Ala Asp	Gly 45 Pro Ser Met Gly Val 125	His 30 Lys Trp Arg Pro Asn 110 Asn	Lys Leu Pro Tyr Glu 95 Tyr Arg	Phe Thr Thr Pro 80 Gly Lys Ile	

	150	155 160	
Lys Gln Lys Asn Gly 165		Lys Ile Arg His Asn Ile 175	
Glu Asp Gly Ser Val 180	Gln Leu Ala Asp His 185	Tyr Gln Gln Asn Thr Pro 190	
Ile Gly Asp Gly Pro 195	Val Leu Leu Pro Asp 200	Asn His Tyr Leu Ser Thr 205	
Gln Ser Ala Leu Ser 210	Lys Asp Pro Asn Glu 215	Lys Arg Asp His Met Val 220	
Leu Leu Glu Phe Val 225	Thr Ala Ala Gly Ile 230	Thr His Gly Met Asp Glu 235 240	
Leu Tyr Lys			
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<221> CDS <222> (1)(732) <400> 109 atg tat tat tat tat Met Tyr Tyr Tyr 1 5 gtc cca att ctc gtg	Tyr Ser Lys Gly Glu 10 gaa ctg gat ggc gat	Glu Leu Phe Thr Gly Val	48 96
<221> CDS <222> (1)(732) <400> 109 atg tat tat tat tat Met Tyr Tyr Tyr 1 5 gtc cca att ctc gtg Val Pro Ile Leu Val 20 tct gtc agc gga gag	Tyr Ser Lys Gly Glu 10 gaa ctg gat ggc gat Glu Leu Asp Gly Asp 25 ggt gaa ggt gat gcc	Glu Leu Phe Thr Gly Val 15 gtg aat ggg cac aaa ttt Val Asn Gly His Lys Phe	
<221> CDS <222> (1)(732) <400> 109 atg tat tat tat tat Met Tyr Tyr Tyr 1 5 gtc cca att ctc gtg Val Pro Ile Leu Val 20 tct gtc agc gga gag Ser Val Ser Gly Glu 35 ctg aaa ttc atc tgc	Tyr Ser Lys Gly Glu 10 gaa ctg gat ggc gat Glu Leu Asp Gly Asp 25 ggt gaa ggt gat gcc Gly Glu Gly Asp Ala 40 acc act gga aag ctc	Glu Leu Phe Thr Gly Val 15 gtg aat ggg cac aaa ttt Val Asn Gly His Lys Phe 30 aca tac gga aag ctc acc Thr Tyr Gly Lys Leu Thr	96
<221> CDS <222> (1)(732) <400> 109 atg tat tat tat tat Met Tyr Tyr Tyr Tyr 1 5 gtc cca att ctc gtg Val Pro Ile Leu Val 20 tct gtc agc gga gag Ser Val Ser Gly Glu 35 ctg aaa ttc atc tgc Leu Lys Phe Ile Cys 50 ctg gtc act acc ttc	Tyr Ser Lys Gly Glu gaa ctg gat ggc gat Glu Leu Asp Gly Asp 25 ggt gaa ggt gat gcc Gly Glu Gly Asp Ala 40 acc act gga aag ctc Thr Thr Gly Lys Leu 55 tct tat ggc gtg cag	Glu Leu Phe Thr Gly Val 15 gtg aat ggg cac aaa ttt Val Asn Gly His Lys Phe 30 aca tac gga aag ctc acc Thr Tyr Gly Lys Leu Thr 45 cct gtg cca tgg cca aca Pro Val Pro Trp Pro Thr	96 144

tat gtg cag Tyr Val Gln			Phe									336
acc cgc gct Thr Arg Ala 115	Glu Val											384
gag ctg aag Glu Leu Lys 130												432
aag ctg gaa Lys Leu Glu 145												480
aag caa aag Lys Gln Lys		_	_	Asn :		_		_				528
gag gat gga Glu Asp Gly			Ala .	_				_				576
atc ggc gac Ile Gly Asp 195	Gly Pro											624
cag tct gcc Gln Ser Ala 210												672
ctg ctg gag Leu Leu Glu 225	Phe Val											720
ctg tac aag Leu Tyr Lys	tga											732
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Val Pro Ile	Leu Val 20	Glu Leu	Asp (Gly <i>1</i> 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	
Ser Val Ser	Gly Glu	Gly Glu	Gly A	Asp A	Ala	Thr	Tyr	Gly 45	Lys	Leu	Thr	

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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115
                            120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
                                        155
                    150
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                                    170
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
                    230
                                        235
Leu Tyr Lys
<210> 111
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<213> Artificial Sequence
<223> Description of Artificial Sequence: Tyr(TAC)5GFP
<220>
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<222> (1) .. (732)
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Met Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                  5
                                                         15
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		att Ile														96
		agc Ser 35														144
		ttc Phe														192
		act Thr														240
		atg Met	-	-		-			_	_	_	_				288
		cag Gln														336
	-	gct Ala 115	_	_	_		_		_		_			_		384
		aag Lys														432
		gaa Glu											_	_	_	480
-		aag Lys				_	_			_		_				528
	_	gga Gly			_	_	_	_				_				576
		gac Asp 195														624
_		gcc Ala	_			_			_	_	_	_		_	_	672
		gag Glu										Gly				720
ctg	tac	aag	tga													732

<210> 112

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<400> 112

Met Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr 195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu 225 230 235 240

Leu Tyr Lys

Lys G	ln	Lys	Asn	Gly 165	Ile	Lys	Val	Asn	Phe 170	Lys	Ile	Arg	His	Asn 175	Ile	
gag g Glu A																576
atc g Ile G																624
cag t Gln S 2																672
ctg c Leu L 225																720
ctg t Leu T		_	tga													732
<210><211><211><212><213>	> 24 > PR	3 T	.cial	L Sec	quenc	ce										
<220> <223>		scri	.ptic	on of	Art	ific	cial	Sequ	ience	e: Va	al (GT	ra) 50	GFP			
	> De	.4												Gly 15	Val	
<223> <400> Met V	→ De → 11 /al	.4 Val	Val	Val 5	Val	Ser	Lys	Gly	Glu 10	Glu	Leu	Phe	Thr	15		
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<223> <400> Met V 1 Val P Ser V Leu L	→ De → 11 Val Pro Val 50	4 Val Ile Ser 35 Phe	Val Leu 20 Gly	Val 5 Val Glu Cys	Val Glu Gly Thr	Ser Leu Glu Thr 55	Lys Asp Gly 40 Gly	Gly Gly 25 Asp	Glu 10 Asp Ala Leu	Glu Val Thr Pro	Leu Asn Tyr Val 60	Phe Gly Gly 45	Thr His 30 Lys Trp	15 Lys Leu Pro	Phe Thr	
<223> <400> Met V 1 Val P Ser V Leu L	→ De → 11 Val Pro → Yal → Ys 50	Val Ile Ser 35 Phe	Val Leu 20 Gly Ile	Val 5 Val Glu Cys	Val Glu Gly Thr Ser 70	Ser Leu Glu Thr 55 Tyr	Lys Asp Gly 40 Gly Gly	Gly Gly 25 Asp Lys	Glu 10 Asp Ala Leu Gln	Glu Val Thr Pro Cys 75	Leu Asn Tyr Val 60 Phe	Phe Gly Gly 45 Pro	Thr His 30 Lys Trp Arg	15 Lys Leu Pro Tyr	Phe Thr Thr Pro 80	
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	135	1	40
Lys Leu Glu Tyr 1 145	Asn Tyr Asn Ser 150	His Asn Val T	yr Ile Met Ala Asp 160
	Gly Ile Lys Val 165	Asn Phe Lys I 170	le Arg His Asn Ile 175
Glu Asp Gly Ser V	Val Gln Leu Ala	ASP His Tyr G	ln Gln Asn Thr Pro 190
Ile Gly Asp Gly I 195	Pro Val Leu Leu 200	=	is Tyr Leu Ser Thr 205
Gln Ser Ala Leu S 210	Ser Lys Asp Pro 215	-	rg Asp His Met Val 20
Leu Leu Glu Phe V 225	Val Thr Ala Ala 230	a Gly Ile Thr H 235	is Gly Met Asp Glu 240
Leu Tyr Lys			
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<pre><221> CDS <222> (1)(732) <400> 115 atg gtc gtc gtc gtc gtc gtc gtc gtc gtc g</pre>	Val Val Ser Lys 5 gtg gaa ctg gat Val Glu Leu Asp gag ggt gaa ggt Glu Gly Glu Gly 40 cgc acc act gga	ggc gat gtg ag ggc gat gtg ag ggc gat gtg ag gc gat gtg ag gc aca tag Asp Ala Thr Ty	eu Phe Thr Gly Val 15 at ggg cac aaa ttt 96 sn Gly His Lys Phe 30 ac gga aag ctc acc 144 yr Gly Lys Leu Thr

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc

Asp H	is	Met	Lys	Gln 85	His	Asp	Phe	Phe	Lys 90	Ser	Ala	Met	Pro	Glu 95	Gly	
tat gi Tyr Va	_	_		_						_	_				_	336
acc co	rg															384
gag ct Glu Le																432
aag ct Lys Le 145	_	_											_	_	_	480
aag ca Lys G																528
gag ga Glu As					_	-	_	_				_				576
atc gg	ly.	_							-				_			624
cag to Gln Se 2:		_	_			_			-	_	_	_		_	_	672
ctg ct Leu Le 225	_						-						-	-		720
ctg ta		_	tga							•				•		732
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Val P	ro	Ile	Leu 20	Val	Glu	Leu	Asp	Gly 25	Asp	Val	Asn	Gly	His 30	Lys	Phe	

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
                     70
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100
                                105
                                                    110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                            120
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                        135
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180
                                185
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                            200
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                        215
                                            220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225
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Leu Tyr Lys
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<222> (1)..(732)
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-		att Ile			_	_	_		-							96
	-	agc Ser 35				_		_	_				_		acc [,] Thr	144
_		ttc Phe		_												192
_	_	act Thr							_				_			240
_		atg Met	_	_		_			_	_	_	_				288
		cag Gln		-						_	_				_	336
	_	gct Ala 115	_	_	_		_		_		_			_		384
		aag Lys														432
_	_	gaa Glu								-			_	_	_	480
		aag Lys														-528
		gga Gly														576
		gac Asp 195														624
		gcc Ala	_			_			_	_	-	_		_	_	672
		gag Glu														720

225 230 235 240

ctg tac aag tga 732 Leu Tyr Lys

<210> 118

<211> 243

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Val(GTG)5GFP

<400> 118

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
35 40 45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50 60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro 65 70 75 80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 90 95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
100 105 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 120 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 135 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp 145 150 155 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile 165 170 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro 180 185 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
195 200 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val 210 215 220

225 Leu Tyr Lys <210> 119 <211> 732 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Val(GTT)5GFP <220> <221> CDS <222> (1)..(732) <400> 119 atg gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt 96 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe 20 25 tet gte age gga gag ggt gaa ggt gat gee aca tae gga aag ete ace 144 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr 35 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr 55 ctg gtc act acc ttc tct tat ggc gtg cag tqc ttt tcc aqa tac cca Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly 85 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys 100 105 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile 115 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His 130 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp

145	150	155	160
	y Ile Lys Val Asn	ttc aag atc aga cac Phe Lys Ile Arg His 170	
		cat tat caa cag aac His Tyr Gln Gln Asn 190	
		gac aac cat tac ctg Asp Asn His Tyr Leu 205	
		gaa aag aga gac cac Glu Lys Arg Asp His 220	
		atc aca cat ggc atg Ile Thr His Gly Met 235	
ctg tac aag tga Leu Tyr Lys			732
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<212> PRT <213> Artificial S <220> <223> Description <400> 120 Met Val Val Val Val 1	of Artificial Seq l Val Ser Lys Gly 5	Glu Glu Leu Phe Thr 10 Asp Val Asn Gly His	15
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115	120	1	125
Glu Leu Lys Gly Il 130	e Asp Phe Lys G 135	Glu Asp Gly Asn 1 140	Ile Leu Gly His
Lys Leu Glu Tyr As 145	n Tyr Asn Ser H 150	Iis Asn Val Tyr 1 155	Ile Met Ala Asp 160
Lys Gln Lys Asn Gl 16		Asn Phe Lys Ile <i>P</i> 170	Arg His Asn Ile 175
Glu Asp Gly Ser Va 180		sp His Tyr Gln (.85	Gln Asn Thr Pro 190
Ile Gly Asp Gly Pr 195	o Val Leu Leu P 200	_	Tyr Leu Ser Thr 205
Gln Ser Ala Leu Se 210	r Lys Asp Pro A 215	asn Glu Lys Arg <i>I</i> 220	Asp His Met Val
Leu Leu Glu Phe Va 225	l Thr Ala Ala G 230	ly Ile Thr His (235	Gly Met Asp Glu 240
Leu Tyr Lys			
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Leu Val Thr 60	Thr Phe	Ser Tyr 65	Gly	Val	Gln	Cys 70	Phe	Ser	Arg	Tyr	Pro 75	
gac cat atg Asp His Met	-	_			_	_	_	_			~~	288
tat gtg cag Tyr Val Gln						_	-				_	336
acc cgc gct Thr Arg Ala 110												384
gag ctg aag Glu Leu Lys 125			Lys		_							432
aag ctg gaa Lys Leu Glu 140									_	_	_	480
aag caa aag Lys Gln Lys												528
gag gat gga Glu Asp Gly												576
atc ggc gac Ile Gly Asp 190												624
cag tct gcc Gln Ser Ala 205		-	Pro		-	_	_	_		_	-	672
ctg ctg gag Leu Leu Glu 220	ttt gtg Phe Val	acc gct Thr Ala 225	gct Ala	gly aaa	atc Ile	aca Thr 230	cat His	ggc Gly	atg Met	gac Asp	gag Glu 235	720
ctg tac aag Leu Tyr Lys	tga											732
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	0> 12 tag		tag	tag	tag									ggc Gly 10			48
														aaa Lys			96
														ctc Leu			144
														cca Pro			192
														tac Tyr			240
_		_	_	_		_			_	_	_	_		gag Glu 90			288
		_								_				tac Tyr	aag Lys	٠.	336
														aga Arg			384
														ggc Gly			432
														gcc Ala			480
		_				_	_			_		_		aac Asn 170			528
														act Thr			576
		_							_				_	tcc Ser			624
cag	tct	gcc	ctg	tct	aaa	gat	ccc	aac	gaa	aag	aga	gac	cac	atg	gtc		672

Gln Ser Ala L 205	=	Asp Pro Asn 210	Glu Lys Arg 215	Asp His Met	Val
ctg ctg gag t Leu Leu Glu P 220					
ctg tac aag t Leu Tyr Lys	ga -				732
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gtc cca att c Val Pro Ile L 1	eu Val Glu I				
tct gtc agc g Ser Val Ser G 30					
ctg aaa ttc a Leu Lys Phe I 45	le Cys Thr T				
ctg gtc act ac Leu Val Thr Ti 60	cc ttc tct t hr Phe Ser 1 65	tat ggc gtg Tyr Gly Val	cag tgc ttt Gln Cys Phe 70	tcc aga tac Ser Arg Tyr	cca 240 Pro 75
gac cat atg a Asp His Met L					
tat gtg cag ga Tyr Val Gln G	lu Arg Thr I				
acc cgc gct ga Thr Arg Ala G 110					

		gag gat gga aac att Glu Asp Gly Asn Ile 135						
		cac aat gtg tac atc His Asn Val Tyr Ile 150						
Lys Gln Lys Asn G		aac ttc aag atc aga Asn Phe Lys Ile Arg 165						
		gac cat tat caa cag Asp His Tyr Gln Gln 180						
		cca gac aac cat tac Pro Asp Asn His Tyr 200	Leu Ser Thr					
	_	aac gaa aag aga gac Asn Glu Lys Arg Asp 215	- -					
		ggg atc aca cat ggc Gly Ile Thr His Gly 230						
ctg tac aag tga Leu Tyr Lys			732					
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		cac aaa ttt tct gtc His Lys Phe Ser Val 25						
		aag ctc acc ctg aaa Lys Leu Thr Leu Lys 45	Phe Ile Cys					

													act Thr			192
													atg Met			240
													cag Gln			288
													gct Ala 110			336
							-		_			_	aag Lys			384
											_	_	gaa Glu			432
													aag Lys			480
													gga Gly			528
							_						gac Asp 190			576
Val	Leu	Leu 195	Pro	Asp	Asn	His	Tyr 200	Leu	Ser	Thr	Gln	Ser 205	gcc Ala	Leu	Ser	624
													gag Glu			672
							ggc						aag Lys	tga		717
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<211> 238

<212> PRT

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<220>

<223> Description of Artificial Sequence: GFP humanized

control

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<220>

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<223> Description of Artificial Sequence: Ala(GCA)5 primer

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      primer
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<223> Description of Artificial Sequence: Asp(GAT)5
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<211> 54
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<223> Description of Artificial Sequence: Gln(CAA)5
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<210> 143
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<212> DNA
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     primer
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<211> 54
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<212> DNA
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<211> 54
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<223> Description of Artificial Sequence: Glu(GAG)5
      primer
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<210> 148
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<210> 149
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<210> 150
<211> 54
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<223> Description of Artificial Sequence: His(CAC)5
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<210> 151
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<223> Description of Artificial Sequence: Ile(ATA)5
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primer

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                                                             54
<210> 154
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<223> Description of Artificial Sequence: Ile(ATT)5
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<211> 54
<212> DNA
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<210> 157
<211> 54
<212> DNA
<213> Artificial Sequence
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<210> 158
<211> 54
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<223> Description of Artificial Sequence: Leu(CTT)5
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<210> 160
<211> 54
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<223> Description of Artificial Sequence: Leu(TTG)5
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<210> 161
<211> 54
<212> DNA
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      primer
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<211> 54
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<211> 54
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